What is claimed is:

1. A method of analyzing a target nucleic acid, comprising:

(a) providing an array of probes comprising a probe set comprising probes complementary to a reference sequence;

(b) hybridizing the target nucleic acid to the array of probes;

(c) determining the relative hybridization of the probes to the target nucleic acid,

(d) estimating the sequence of the target nucleic acid from the relative hybridization of the probes;

(e) providing a further array of probes comprising a probe set comprising probes complementary to the estimated sequence of the target nucleic acid;

(f) hybridizing the target nucleic acid to the further array of probes;

(g) determining the relative hybridization of the probes to the target nucleic acid;

(h) reestimating the sequence of the target nucleic acid from the relative hybridization of the probes.

2. The method of claim 1, further comprising repeating steps (e)-(h) as necessary until the reestimated sequence of the target nucleic acid is the true sequence of the target nucleic acid.

3. The method of claim 1, wherein the target nucleic acid is a species variant of the reference sequence.

4. The method of claim 1, wherein the reference sequence is from a human and the target nucleic acid is from a primate.

5. The method of claim 1, wherein the target nucleic acid shows 50-99% sequence identity with the reference sequence.

6. The method of claim 1, wherein the target nucleic acid shows 80-95% sequence identity with the reference sequence.

7. The method of claim 1, wherein the reference sequence is at least 1000 nucleotides long, the array comprises a probe set comprising overlapping probes that are perfectly complementary to and span the reference sequence, and the further array comprises probes that are perfectly complementary to and span the estimated sequence.

8. The method of claim 1, wherein an estimated sequence of the target nucleic acid includes a position of ambiguity and the probe set showing perfect complementarity to the estimated sequence includes a probe having including a pooled nucleotide aligned with the position of ambiguity in the target sequence.

9. The method of claim 1, wherein the reference sequence is at least 10 kb.

10. The method of claim 1, wherein the reference sequence is at least 1000 kb.

11. The method of claim 1, wherein the reference sequence includes at least 90% of the human genome.

12. The method of claim 1, wherein the array of probes comprises:

(1) a first probe set comprising a plurality of probes, each probe comprising a segment of at least six nucleotides exactly complementary to a subsequence of the reference sequence, the segment including at least one interrogation position complementary to a corresponding nucleotide in the reference sequence,

(2) second, third and fourth probe sets, each comprising a corresponding probe for each probe in the first probe set, the probes in the second, third and fourth probe

sets being identical to a sequence comprising the corresponding probe from the first probe set or a subsequence of at least six nucleotides thereof that includes the at least one interrogation position, except that the at least one interrogation position is occupied by a different nucleotide in each of the four corresponding probes from the four probe sets.

13. The method of claim 12, wherein the sequence of the target nucleic acid is estimated by:

(a) comparing the relative specific binding of four corresponding probes from the first, second, third and fourth probe sets;

(b) assigning a nucleotide in the sequence of the target nucleic acid as the complement of the interrogation position of the probe having the greatest specific binding;

(c) repeating (a) and (b) until each nucleotide of interest in the sequence of the target nucleic acid has been estimated.

14. The method of claim 1, wherein the sequence of the target nucleic acid differs from the reference by at least two positions within a probe length.

15. A method of analyzing a target nucleic acid, comprising:

(a) designing an array of probes to be complementary to an estimated sequence of the target nucleic acid,

(b) hybridizing the array of probes to the target nucleic acid;

(c) determining a reestimated sequence of the target nucleic acid from the hybridization pattern of the array to the target nucleic acid sequence to; and

(d) repeating (a)-(c) at least once.